

SEQUENCE LISTING

<110> Rhone-Poulenc Agro; Betzner, Andreas Stefan; Doutriaux,
Marie-Pascale; Freyssinet, Georges; Perez, Pascual.

<120> Methods for obtaining plant varieties

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<223> Degenerate oligonucleotides UPMU used to isolate AtMSH3 and
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<301> Reenan and Kolodner

<302> Genetics

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<307> 1992

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Met Gly Lys Gln Lys Gln Gln Thr Ile Ser Arg Phe Phe Ala Pro Lys
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Pro Lys Ser Pro Thr His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr
20 25 30

ccg cca ccg aag ata tcc gcc act gta tcc ttc tct cct tcc aag cgt 243
Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg
35 40 45

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Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys
50 55 60

ctt tct cct cac act caa aac cca gta ccc gat ccc aat tta cac caa 339
Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
65 70 75 80

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Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro	
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gaa acg tca tca tcg agg aaa tac aca cca ttg gaa cag caa gtg gtg	435
Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val	
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gag cta aag agc aag tac cca gat gtg gtt ttg atg gtg gaa gtt ggt	483
Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly	
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Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val	
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Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val	
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Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly	
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Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser	
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His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu	
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Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys	
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Val Asp Glu Arg Val Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met	
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 Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn
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 Gly Asn Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala
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 Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys
 355 360 365

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 Phe Glu Arg Ile Leu Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Ser
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 Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val
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 Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn
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 Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp
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 Lys Ala Thr Glu Phe Ile Ala Val Met Glu Ala Ile Leu Leu Ala Gly
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gtt tta gtc atc agg gaa aag ctg gat tcc tcg ata gct tca ttt cgc 2067
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aca cat ttg ata gag ctg ccc gtt gat tcc aag gtc cct atg aat tgg 2163
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 675 680 685

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 690 695 700

004221 6626560

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Tyr Tyr Thr Asp Phe Lys Ala Ala Val Gln Ala Leu Ala Ala Leu Asp	
740 745 750	
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Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg	
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Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser	
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Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro	
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Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu	
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Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala	
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 Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly
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 Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg
 965 970 975

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 Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln
 980 985 990

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 Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu
 995 1000 1005

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 Ile Arg Leu Lys Pro Thr Cys Ser Phe
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35 40 45

Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys
50 55 60

Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
65 70 75 80

Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro
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Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val
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Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly
115 120 125

Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val
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Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val
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Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly
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Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser
180 185 190

His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu
195 200 205

Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys
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225 230 235 240

Val Asp Glu Arg Val Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met
245 250 255

[illegible]

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 Pro Leu Ser Gln Gln Thr Glu Lys Phe Leu Val Ala Met Ala Gly Pro
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 Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn
 325 330 335
 Gly Asn Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala
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 Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys
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 Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu
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 Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn
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 Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp
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 Leu Ser Ser Glu Leu Val Glu Glu Gly Ser Glu Arg Ala Ile Val Ser
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 Val Ile Ser Ser Pro Val Val Val Asp Asn Ala Gly Lys Leu Leu Ser
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 Ala Leu Asn Lys Glu Ala Ala Val Arg Gly Asp Leu Leu Asp Ile Leu
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 Ile Thr Ser Ser Asp Gln Phe Pro Glu Leu Ala Glu Ala Arg Gln Ala
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 Lys Lys Leu Ala Ile Arg Asn Leu Glu Phe Leu Gln Val Ser Gly Ile
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 Thr His Leu Ile Glu Leu Pro Val Asp Ser Lys Val Pro His Asn Trp
 675 680 685
 Val Lys Val Asn Ser Thr Lys Lys Thr Ile Arg Tyr His Pro Pro Glu
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 Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser
 770 775 780
 Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro
 785 790 795 800
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 Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu
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 Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr
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 Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly
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 Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg
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 Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln
 980 985 990
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tctgtcgatg aggttagagg aacggatact ccaccggaga aggttccgcg tcgtgtcctg 240

ccgtctggat ttaagccggc tgaatccgcc ggtgatgctt cgtccctggt ctccaatatt 300

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gttgttccgc tgaatgattc atctctatgt atgaaggcta atgatgttat tcctcaattt 420

cgtrccaata atggtaaaac tcaagaaaga aaccatgctt ttagtttcag tgggagagct 480

gaacttagat cagtagaaga tataggagta gatggcgatg ttcttgggtcc agaaacacca 540

gggatgcgctc cacgtgcttc tcgcttgaag cgagttctgg aggatgaaat gacttttaag 600

gaggataagg ttctctgtatt ggactctaac aaaaggctga aaatgctcca ggatccgggtt 660

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 <223> Clone 62

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<210> 29
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tctctctcac aattccaaaa a atg cag cgc cag aga tcg att ttg tct ttc 171
 Met Gln Arg Gln Arg Ser Ile Leu Ser Phe
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23

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Phe Gln Lys Pro Thr Ala Ala Thr Thr Lys Gly Leu Val Ser Gly Asp	
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Ala Ala Ser Gly Gly Gly Gly Ser Gly Gly Pro Arg Phe Asn Val Arg	
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Glu Gly Asp Ala Lys Gly Asp Ala Ser Val Arg Phe Ala Val Ser Lys	
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Ser Val Asp Glu Val Arg Gly Thr Asp Thr Pro Pro Glu Lys Val Pro	
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cgt cgt gtc ctg ccg tct gga ttt aag ccg gct gaa tcc gcc gst gat	411
Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp	
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Ala Ser Ser Leu Phe Ser Asn Ile Met His Lys Phe Val Lys Val Asp	
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Asp Arg Asp Cys Ser Gly Glu Arg Ser Arg Glu Asp Val Val Pro Leu	
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Asn Asp Ser Ser Leu Cys Met Lys Ala Asn Asp Val Ile Pro Gln Phe	
125 130 135	
cgt tcc aat aat ggt aaa act caa gaa aga aac cat gct ttt agt ttc	603
Arg Ser Asn Asn Gly Lys Thr Gln Glu Arg Asn His Ala Phe Ser Phe	
140 145 150	
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Ser Gly Arg Ala Glu Leu Arg Ser Val Glu Asp Ile Gly Val Asp Gly	
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Asp Val Pro Gly Pro Glu Thr Pro Gly Met Arg Pro Arg Ala Ser Arg	
175 180 185	
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Leu Lys Arg Val Leu Glu Asp Glu Met Thr Phe Lys Glu Asp Lys Val	
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cct gta ttg gac tct aac aaa agg ctg aaa atg ctc cag gat ccg gtt	795
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205 210 215	

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25

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Lys Glu Val Leu Tyr Asp Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys	
445 450 455	
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Ala Leu Arg Lys Tyr Thr Leu Thr Gly Ser Thr Ala Val Gln Leu Ala	
460 465 470	
cca gta cca caa gta atg ggg gat aca gat gct gct gga gtt aga aat	1611
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Lys His Gly Asp Ile Phe Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg	
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620 625 630	

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 685 690 695

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 735 740 745

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 750 755 760

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 765 770 775

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 780 785 790

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 795 800 805 810

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004227 622550

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			100					105					110		
Glu	Arg	Ser	Arg	Glu	Asp	Val	Val	Pro	Leu	Asn	Asp	Ser	Ser	Leu	Cys
		115					120					125			

Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys
 130 135 140
 Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu
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 Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu
 165 170 175
 Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu
 180 185 190
 Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn
 195 200 205
 Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu
 210 215 220
 Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg
 225 230 235 240
 Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr
 245 250 255
 Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys
 260 265 270
 Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe
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 Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly
 290 295 300
 His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys
 305 310 315 320
 Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys
 325 330 335
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 Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys
 355 360 365
 Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly
 370 375 380
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 385 390 395 400
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002207-622550

Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys
690 695 700

Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln
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 Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp
 725 730 735
 Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe
 740 745 750
 Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys
 755 760 765
 Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly
 770 775 780
 Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln
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 Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile
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 835 840 845
 Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg
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 Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu
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 Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu
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 Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys
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 Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser
 980 985 990

002207 66262660
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32

Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu
995 1000 1005

Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln Val
1010 1015 1020

Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly
1025 1030 1035 1040

Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe Lys Ser Ser
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Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp Trp Leu Lys Ser
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Leu Val Gly Ile Ser Arg Val Ala His Asn Asn Ala Pro Ile Gly Glu
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Tyr Cys Val Pro Lys
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<400> 33

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<210> 34
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<400> 34

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38

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<210> 44
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aaccaaggca cagaagcg

18

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09520239 102700

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gcacataccc acaaccagaa 20

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aaagagatga gaatttggac 20

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18

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Arabidopsis thaliana subspecies

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in Arabidopsis thaliana subspecies

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tgacctcctc ttccatggag

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in Arabidopsis thaliana subspecies
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in Arabidopsis thaliana subspecies

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in Arabidopsis thaliana subspecies

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Arabidopsis thaliana subspecies

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Arabidopsis thaliana subspecies

<400> 67
catccgaatg ccattgttc 19

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00420T 622550

<223> Forward primer for PCR amplification of NGA126 SSLP marker in
Arabidopsis thaliana subspecies

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gaaaaaacgc tacttttcgtg g 21

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<211> 22

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<223> Reverse primer for PCR amplification of NGA126 SSLP marker in
Arabidopsis thaliana subspecies

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caagagcaat atcaagagca gc 22

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<212> DNA

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<223> Forward primer for PCR amplification of NGA162 SSLP marker in
Arabidopsis thaliana subspecies

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catgcaattt gcatctgagg 20

<210> 71

<211> 22

<212> DNA

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<223> Reverse primer for PCR amplification of NGA162 SSLP marker in
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Arabidopsis thaliana subspecies
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in Arabidopsis thaliana subspecies

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in *Arabidopsis thaliana* subspecies

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<223> Reverse primer for PCR amplification of NGA225 SSLP marker in
Arabidopsis thaliana subspecies

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<223> Forward primer for PCR amplification of NGA249 SSLP marker in
Arabidopsis thaliana subspecies

<400> 82

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19

<210> 83

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Arabidopsis thaliana subspecies

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ggatccctaa ctgtaaaatc cc

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<210> 84

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<223> Forward primer for PCR amplification of CA72 SSLP marker in
Arabidopsis thaliana subspecies

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<210> 85

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Arabidopsis thaliana subspecies

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cccagtctaa ccacgaccac

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<210> 86

<211> 20

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Arabidopsis thaliana subspecies

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<210> 87

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<223> Reverse primer for PCR amplification of NGA151 SSLP marker in
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<210> 90

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<223> Forward primer for PCR amplification of NGA139 SSLP marker in
Arabidopsis thaliana subspecies

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<210> 91

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aggcatggga gacatttacg 20

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in Arabidopsis thaliana subspecies

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ctccaccaat catgcaaag 20

09529239-102700

<210> 95
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 in Arabidopsis thaliana subspecies

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<210> 97
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